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Animal Industry Report

Animal Industry Report

AS 651

ASL R2038

2005

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Recommended Citation

Serenius, T. and Stalder, Kenneth J. (2005) "Genetics of Sow Longevity," *Animal Industry Report*: AS 651, ASL R2038.

DOI: https://doi.org/10.31274/ans_air-180814-1076

Available at: https://lib.dr.iastate.edu/ans_air/vol651/iss1/19

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Genetics of Sow Longevity

A.S. Leaflet R2038

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Summary and Implications

The objective of this study was to estimate direct and indirect selection potential for length of productive life and lifetime prolificacy. In order to study the direct selection potential, the heritabilities of these traits were estimated. The genetic correlations of length of productive life and lifetime prolificacy with prolificacy traits and overall leg conformation were estimated to evaluate if selection for these traits could indirectly improve measures of sow longevity. In addition, correlations between length of productive life, lifetime prolificacy, daily gain, and backfat thickness were estimated. Records were utilized from Finnish purebred Landrace (n=26,744) and Large White (n=24,007) sows born on operations that perform on-farm production tests on all females. Heritabilities were estimated using both a survival analysis procedure and a linear model. Due to computational limitations, correlations were estimated with the linear model only. Estimated length of productive life heritabilities obtained from linear model analyses were lower (0.05 to 0.10) than those obtained from survival analyses (0.16 to 0.19). This may be indicative of the superiority of survival analysis compared to linear model analysis methods when evaluating longevity or similar types of data. All the prolificacy traits were genetically correlated with length of productive life and lifetime prolificacy and the correlations were greater than 0.13. These results indicate that selection for increased number of piglets weaned in the first litter and for short first farrowing interval is beneficial for sow longevity and also for sow's lifetime prolificacy. The genetic correlations between length of productive life and leg conformation score were also favorable (0.32 in Landrace and 0.17 in Large White). The heritability estimates indicate that survival analysis is likely the most appropriate method of evaluating longevity traits in swine. Because of computational problems, simultaneous analysis of linear traits and longevity is not currently possible. More research is needed to develop methods for multiple linear and survival trait analyses.

Introduction

Prolificacy traits and longevity play an important role in efficient piglet production. Lifetime prolificacy (LTP) is related to longevity of the sow as the higher number of parities the sow remains in the herd, the higher likelihood of an increased number of piglets she will produce during her productive lifetime. Higher replacement rates due to poor longevity increase the number of replacement gilts needed and the associated expenses related to purchase or raising of those gilts.

To compare the efficiency of direct and indirect selection for sow longevity, the genetic parameters

(heritabilities, genetic correlations) should be known. The effectiveness of indirect and direct selection for swine longevity traits is likely population dependent and should be evaluated before selection is actually implemented. Information regarding the effectiveness of direct and indirect selection potential for sow longevity is sparse. Genetic correlations between sow longevity and other economically important swine traits are needed to determine the importance of their association.

Materials and Methods

Data obtained from the Finnish Animal Breeding Association (FABA) (Vantaa, Finland) were used to estimate the genetic parameters for length of productive life (LPL) and lifetime prolificacy (LTP). Additionally, daily gain (ADG; 0 to 100 kg), body composition (backfat thickness) measured with ultrasound, age at first farrowing (AFF), first farrowing interval (FFI), number of weaned piglets at first farrowing (NW), and leg score data were captured in order to estimate genetic and phenotypic correlations of these traits with LPL and LTP.

Both, single trait proportional hazard model, and multi trait linear model were fitted to the current data. The single trait analyses were carried out with the Survival Kit (Ducrocq and Solkner, 2001), and multi trait analyses with DMU package (Madsen and Jensen, 2000). Two separate longevity analyses were carried out for both the breeds. The first was targeted to approximate true LPL, and thus, fixed time dependent farm-year and random genetic sire effects were the only effects included in the statistical model. In addition to these effects, the fixed effects of leg score (1 to 5), number of weaned piglets in first litter, and a regression of age at first farrowing were also included in the statistical model to approximate functional LPL.

In linear model analysis, the censored records (sows sold or still alive) of LPL and LTP were treated as missing. The fixed effect of farm and year interaction was included in the statistical model for all of the traits studied. In addition, farrowing month (NW, AFF, ADG, backfat thickness, leg score), mating type (NW), age of litter at weaning (NW, FFI), and breeding consultant (ADG, fat-%, leg score) were the other effects included in. Moreover, the fixed regression of test weight was included in the statistical models for ADG and fat-%.

Results and Discussion

Three different heritability estimates for LPL, for Finnish Landrace and Large White breeds, are presented in Table 1. In general, all the estimates were very similar between the breeds. The heritabilities obtained from linear model analysis (0.05 in Landrace and 0.10 in Large White) were lower than those obtained from the survival analysis (0.16 to 0.17 in Landrace and 0.17 to 0.19 in Large White). In addition, the difference between the breeds was greater in the

linear model analyses when compared to those obtained from the survival analyses. In linear model analysis, the estimated heritabilities for LTP (0.09 in Landrace and 0.12 in Large White) were slightly higher than those for LPL (Tables 2 and 3).

Table 1. Heritability estimates for length of productive life (LPL) obtained from survival analysis and multi-trait linear model analysis in the Finnish Landrace (LR) and Large White (LW) populations.

	LR	LW
Survival		
True LPL, d	0.16	0.17
Functional LPL, d	0.17	0.19
Linear model		
Linear LPL, d	0.05	0.10

Current heritability estimates indicate that environmental effects may be modeled more precisely in survival analysis when compared to the linear model analysis (i.e., it may be assumed that the higher heritability estimates are due to the possibility to model farm-year effect as time dependent). On the other hand, it should be remembered that the residual variance was not estimated in the survival analysis, and the heritability estimates were calculated assuming that the residual effects were following extreme value distribution with the variance ($\pi^2/6$). Therefore, one might argue that the different heritability estimates are not comparable.

Genetic and phenotypic correlations are presented in tables 2 and 3. In general, phenotypic correlations were very similar between the breeds, whereas some genetic correlations differed between breeds. Moreover, the phenotypic correlations were commonly very low. However, there was an indication that LPL and LTP are very closely associated, as both phenotypic and genetic correlations were greater than 0.90. Because of that, the correlations with the other traits studied are very similar between LPL and LTP.

All the prolificacy traits were genetically correlated with LPL and LTP and the correlations were generally greater than 0.13 (Tables 2 and 3). This indicates that selection for more piglets weaned in the first litter and for short first farrowing interval will have a beneficial indirect

effect for LTP, and for LPL. The absolute values of these genetic correlations ranged between 0.30 and 0.54 and were similar between the Landrace and Large White populations. However, genetic correlation differences for AFF with LTP and LPL were found between the breeds. In Landrace, the correlations were positive (0.17 with LPL and 0.13 with LTP), whereas they were negative in Large White (-0.28 with LPL and -0.29 with LTP).

The genetic correlations between overall leg score and longevity (0.32 with LPL and 0.28 with LTP, Table 2) were moderately positive in Landrace. The corresponding correlations in Large White were 0.17 and 0.19 (Table 3). Although the correlations of overall leg action with LPL and LTP were low to moderate, it may be said that selection for leg conformation, measured when the sow has reached 100 kg, is beneficial for improving sow longevity in an indirect manner.

Based on heritability estimates, it appears that survival analysis may be the most appropriate method of evaluating swine longevity traits compared to linear models. However, there is one major concern relating to the use of survival analysis in breeding value estimation: because of computational problems, multiple trait analyses involving longevity and other economically important traits are not currently possible. As stated earlier, LPL and LTP have genetic correlations with litter size, farrowing interval and leg conformation that are relatively high when compared to genetic correlations among longevity and measures of leg soundness.

Literature Cited

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Table 2. Linear model heritability estimates (\pm SE; diagonal), genetic (\pm SE; above the diagonal) and phenotypic (below the diagonal) correlations between sow efficiency related traits in the Finnish Landrace pigs.

Traits ^a	LPL	LTP	NW	AFF	FFI	ADG	Fat	Score
LPL	0.05 \pm 0.01	0.96 \pm 0.02	0.39 \pm 0.16	0.17 \pm 0.13	-0.43 \pm 0.16	-0.08 \pm 0.12	-0.02 \pm 0.14	0.32 \pm 0.17
LTP	0.94	0.09 \pm 0.01	0.54 \pm 0.12	0.13 \pm 0.11	-0.39 \pm 0.15	-0.05 \pm 0.11	-0.00 \pm 0.11	0.28 \pm 0.14
NW	0.12	0.22	0.06 \pm 0.01	0.01 \pm 0.11	-0.14 \pm 0.16	0.27 \pm 0.10	-0.06 \pm 0.12	-0.15 \pm 0.15
AFF	-0.05	-0.04	0.08	0.47 \pm 0.04	0.25 \pm 0.12	-0.45 \pm 0.06	-0.18 \pm 0.07	-0.37 \pm 0.11
FFI	-0.01	-0.07	0.07	-0.00	0.06 \pm 0.01	-0.04 \pm 0.12	-0.24 \pm 0.13	-0.14 \pm 0.16
ADG	0.01	0.02	0.03	-0.20	-0.02	0.40 \pm 0.03	0.32 \pm 0.06	-0.13 \pm 0.11
Fat	0.01	0.02	0.02	-0.06	-0.04	0.40	0.32 \pm 0.03	0.18 \pm 0.12
Score	0.04	0.04	0.02	-0.01	-0.01	-0.02	0.03	0.06 \pm 0.01

^a LPL = length of productive life, LTP = lifetime prolificacy, AFF = age at first farrowing, FFI = first farrowing interval, NW = number of weaned piglets, ADG = average daily gain between 0 and 100 kg, Fat = backfat thickness at 100 kg of live weight, Score = overall leg action score.

Table 3. Linear model heritability estimates (\pm SE; diagonal), genetic (\pm SE; above the diagonal) and phenotypic (below the diagonal) correlations between sow efficiency related traits in the Finnish Large White pigs

Traits ^a	LPL	LTP	NW	AFF	FFI	ADG	Fat	Score
LPL	0.10 \pm 0.02	0.97 \pm 0.01	0.30 \pm 0.16	-0.28 \pm 0.11	-0.40 \pm 0.18	-0.02 \pm 0.12	0.22 \pm 0.12	0.17 \pm 0.16
LTP	0.94	0.12 \pm 0.02	0.43 \pm 0.14	-0.29 \pm 0.11	-0.35 \pm 0.18	-0.04 \pm 0.11	0.22 \pm 0.11	0.19 \pm 0.16
NW	0.12	0.22	0.06 \pm 0.01	0.21 \pm 0.14	0.12 \pm 0.19	-0.01 \pm 0.14	0.03 \pm 0.14	0.12 \pm 0.19
AFF	-0.08	-0.07	0.07	0.39 \pm 0.03	0.55 \pm 0.13	-0.35 \pm 0.08	-0.09 \pm 0.09	0.07 \pm 0.14
FFI	0.01	-0.03	0.06	0.02	0.04 \pm 0.01	-0.16 \pm 0.14	-0.34 \pm 0.15	0.21 \pm 0.17
ADG	-0.00	-0.00	0.02	-0.19	-0.01	0.40 \pm 0.03	0.39 \pm 0.08	-0.33 \pm 0.13
Fat	0.02	0.02	0.01	-0.06	-0.02	0.40	0.30 \pm 0.03	-0.00 \pm 0.14
Score	0.04	0.04	0.01	-0.01	0.00	-0.02	0.05	0.07 \pm 0.01

^aLPL = length of productive life, LTP = lifetime prolificacy, AFF = age at first farrowing, FFI= first farrowing interval, NW = number of weaned piglets, ADG = average daily gain between 0 and 100 kg, Fat = backfat thickness at 100 kg of live weight, Score = overall leg action score.